## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT:
    - (A) NAME: EUROGENE LIMITED
    - (B) STREET: Marquis House, 67/68 Jermyn Street
    - (C) CITY: London
    - (D) STATE: N/A
    - (E) COUNTRY: United Kingdom
    - (F) POSTAL CODE (ZIP): SW1Y 6NY
  - (ii) TITLE OF INVENTION: THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY FOR THE TREATMENT OF INTIMAL HYPERPLASIA
  - (iii) NUMBER OF SEQUENCES: 10
  - (iv) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
    - (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO (not yet known)

- (2) INFORMATION FOR SEQ ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..441

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG	AAC	TTT	CTG	CTG	TCT	TGG	GTG	CAT	TGG	AGC	CTC	GCC	TTG	CTG	CTC	48
Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu	
1				5					10					15		
										•						
TAC	CTC	CAC	CAT	GCC	AAG	TGG	TCC	CAG	GCT	GCA	CCC	ATG	GCA	GAA	GGA	96
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly	
			20					25					30			
											ATG					144
Gly	Gly		Asn	His	His	Glu		Val	Lys	Phe	Met	_	Val	Tyr	Gln	
		35					40					45				
~~~		m> a	ma.a	~ » m		<b>&gt;</b> ma	030	200	omo.	ama	~~~	<b>&gt;</b> ma	mma	~>~	a	100
											GAC					192
Arg		Tyr	Cys	HIS	Pro		GIU	THE	rea	vai	Asp	ile	Pne	GIN	GIU	
	50					55					60			-		
ጥአሮ	CCT	CAT	CAC	እ ጥር	GAG	ሞልሮ	ልጥሮ	ጥጥር	AAC	CCA	TCC	TOT	GTG.	CCG	CTC	240
											Ser					240
65	FIO	rsħ	GIU	116	70	1 9 1	116	rne	цуз	75	Set	Суз	Vai	FIO	80	•
05					, 0					, ,					-	
ATG	CGA	TGC	GGG	GGC	TGC	TGC	ААТ	GAC	GAG	GGC	CTG	GAG	TGT	GTG	ccc	288
											Leu					
	J	•	_	85	•	•		•	90				•	95		
ACT	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	ATC	AAA	CCT	CAC	336
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His	
			100					105					110		~	
CAA	GGC	CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	CAC	AAC	AAA	TGT	384
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	
		115	·. ·				120					125				
GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	AAA	TGT	GAC	AAG	432
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Càa	Asp	Lys	
	130					135					140					
CCG	AGG	CGG														441
Pro	Arg	Arg														
145																

- (2) INFORMATION FOR SEQ ID NO: 2:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys 130 135 140

Pro Arg Arg

- (2) INFORMATION FOR SEQ ID NO: 3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 573 base pairs

96

144

	55															
		(	c) s	TRANI	DEDN	leic ESS: lin	sin								.`	
	(ii	) MO	LECU:	LE T	YPE:	CDN	A.									
	(iii	) HY	POTH	ETIC	AL: 1	NO										
	(iv	) AN	ri-si	ENSE	: NO						٠					
	•	(1	A) Ni B) Lo	AME/I	ION:	CDS		SEQ :	ID NO	o: 3	<b>:</b>					
ATG	AAC	TTT	CTG	CTG	TCT	TGG	GTG	CAT	TGG	AGC	CTC	GCC	TTG	CTG	CTC	
Met	Asn	Phe 150	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala 160	Leu	Leu	Leu	
TAC	СТС	CAC	CAT	GCC	AAG	TGG	TCC	CAG	GCT	GCA	ccc	ATG	GCA	GAA	GGA:	
			His											Glu		
CCA				<sub>ርን</sub> ሞ	CAC		CTC	CTC	AAC	ጥጥር		CAT	GTC.	TAT	CAC	
														Tyr		
180	1	··			185				-1-	190	-	2	-	-1-	195	
CGC	AGC	TAC	TGC	CAT	CCA	ATC	GAG	ACC	CTG	GTG	GAC	ATC	TTC	CAG	GAG	

CGC AGC T. 192 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu 200 205 210

TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCG CTG 240 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu 220 215 225

ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG TGT GTG CCC 288 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro 230 235 240

ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC AAA CCT CAC 336 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His 250 255 245

CAA	GGC	CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	CAC	AAC	AAA	TGT	384
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	
260					265					270					275	
GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	AAA	CCC	TGT	GGG	432
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Pro	Cys	Gly	
				280					285					290		
CCT	TGC	TCA	GAG	CGG	AGA	AAG	CAT	TTG	TTT	GTA	CAA	GAT	CCG	CAG	ACG	480
Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr	
			295					300					305			
TGT	AAA	TGT	TCC	TGC	AAA	AAC	ACA	GAC	TCG	CGT	TGC	AAG	GCG	AGG	CAG	528
Сув	ГЛа	CÀa	Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys	Lys	Ala	Arg	Gln	
		310					315					320				
CTT	GAG	TTA	AAC	GAA	CGT	ACT	TGC	AGÃ	TGT	GAC	AAG	CCG	AGG	CGG		573
Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg	Cys	Asp	Lys	Pro	Arg	Arg		
	325					330					335					
(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10: 4	:								

- - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 191 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly

Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln 40

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu 65 70 75

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Pro Cys Gly
130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg 180 185 190

- (2) INFORMATION FOR SEQ ID NO: 5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 645 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..645
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

													•		_	
Met	Asn	Phe	Leu 195	Leu	Ser	Trp	Val	His 200	Trp	Ser	Leu	Ala	Leu 205	Leu	Leu	
																0.6
											CCC					96
Tyr	Leu		His	Ala	Lys	Trp		GIn	Ala	Ala	Pro	met 220	Ala	GIU	GIY	
		210					215					220				
GGA	GGG	CAG	AAT	CAT	CAC	GAA	GTG	GTG	AAG	TTC	ATG	GAT	GTC	TAT	CAG	144
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln	
	225					230					235					
CGC	AGC	TAC	TGC	CAT	CCA	ATC	GAG	ACC	CTG	GTG	GAC	ATC	TTC	CAG	GAG	192
											Asp					
240		•	•		245					250	_				255	
											TCC					240
Tyr	Pro	Asp	Glu		Glu	Tyr	Ile	Phe		Pro	Ser	Cys	Val		Leu	
				260					265					270		
ATG	CGA	TGC	GGG	GGC	TGC	TGC	AAT	GAC	GAG	GGC	CTG	GAG	TGT	GTG	ccc	288
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro	
			275					280					285			
ACT	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	ATC	AAA	CCT	CAC	336
											Arg				,	
	•	290	-				295					300				
						•										
											CAG					384
Gln	_	Gln	His	Ile	Gly		Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	
	305					310					315					
GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	AAA	AAA	TCA	GTT	432
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Lys	Ser	Val	
320					325					330					335	
CCA	CCA	B B C	CCN	N N C	ccc	ת תים	מממ	CCA	D D C'	CCC	AAG	מממ	TCC	ccc	ጥአጥ	480
											Lys					400
nrg	Gry	Lys	Gly	340	O. J	<b>J</b> 2	_,_	g	345	9	2,0	2,0	001	350	- , -	
AAG	TCC	TGG	AGC	GTG	ccc	TGT	GGG	CCT	TGC	TCA	GAG	CGG	AGA	AAG	CAT	528
Lys	Ser	Trp	Ser	Val	Pro	Сув	Gly	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	
			355					360					365			
ጥጥር	ጥጥጥ	CTA	ממי	שמט	ccc	ראכ	A CC	ጥርጥ	תממ	ጥርጥ	TCC	ጥርር	מממ	ממ	ACA	576
116	TII	GIM	CMM	GWI	CCG	CAG	ACG	IGT	nnn	161	100	130	AAA	AAC	ACA	3,0

Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr
		370					375					380			

GAC TCG CGT TGC AAG GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC 624

Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys

385 390 395

AGA TGT GAC AAG CCG AGG CGG

Arg Cys Asp Lys Pro Arg Arg

400 405

- (2) INFORMATION FOR SEQ ID NO: 6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 215 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Ser Arg Tyr 145 150 155 160

Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His
165 170 175

Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr 180 185 190

Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys 195 200 205

Arg Cys Asp Lys Pro Arg Arg 210 215

- (2) INFORMATION FOR SEQ ID NO: 7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 696 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1...696
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTC GCC TTG CTC

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu

220 225 230

WO 98/20027 PCT/GB97/03015

								_	_	Οl							
T.F	4C	CTC	CAC	CAT	GCC	AAG	TGG	TCC	CAG	GCT	GCA	ccc	ATG	GCA	GAA	GGA	96
ту	ŗr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly	
				235					240					245			
			-														
GG	SA.	GGG	CAG	AAT	CAT	CAC	GAA	GTG	GTG	AAG	TTC	ATG	GAT	GTC	TAT	CAG	144
G1	У	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln	
			250					255				•	260				
				TGC													192
Ar	g		Tyr	Cys	His	Pro		Glu	Thr	Leu	Val		IIe	Pne	GIn	GIu	
		265					270					275					
מים		ССТ	Chm	GAG	አጥሮ	CAC	ጥልሮ	እጥ <b>ር</b>	ተጥር	AAG	CCA	ጥርር	ጥርጥ	GTG	CCG	СТС	240
-				Glu													240
28			nsp	G <sub>1</sub> u	110	285	- 7 -			2,5	290	5.2		~		295	
AT	CG.	CGA	TGC	GGG	GGC	TGC	TGC	AAT	GAC	GAG	GGC	CTG	GAG	TGT	GTG	CCC	288
Me	et	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro	
		_	-		300	_				305					310		
								-									
AC	T	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	ATC	AAA	CCT	CAC	336
Th	ır	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His	
				315					320					325			
				CAC													384
Gl	.n	Gly		His	Ile	Gly	Glu		Ser	Phe	Leu	Gln		Asn	Lys	Cys	
			330					335					340				
<b>C</b> 2		mc c	202	CCN	220	222	ሮአጥ	202	CCN	מכמ	C A A	ממכ	מממ	מממ	ጥርን	CTT	432
				CCA Pro													432
Gı	·u	345	ALG	PIO	гуs	гåэ	350	rra	NIG	ALG	GIII	355	БYЗ	Буз	261	Val	
		343					330					555					
CG	A	GGA	AAG	GGA	AAG	GGG	CAA	AAA	CGA	AAG	CGC	AAG	AAA	TCC	CGG	TAT	480
				Gly													
36	-	-	-	•	-	365		_	_	_	370	_	_		_	375	
AA	١G	TCC	TGG	AGC	GTG	TAC	GTT	GGT	GCC	CGC	TGC	TGT	CTA	ATG	CCC	TGG	528
Ly	7 S	Ser	Trp	Ser	Val	Tyr	Val	Gly	Ala	Arg	Cys	Cys	Leu	Met	Pro	Trp	
					380					385					390		
AG	C	CTC	CCT	GGC	CCC	CAT	CCC	TGT	GGG	CCT	TGC	TCA	GAG	CGG	AGA	AAG	576
Se	r	Leu	Pro	Gly	Pro	His	Pro	Cys		Pro	Cys	Ser	Glu		Arg	Lys	
				395					400					405			

									62							
CAT	TTG	TTT	GTA	CAA	GAT	CCG	CAG	ACG	TGT	AAA	TGT	TCC	TGC	AAA	AAC	624
His	Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Сув	Ser	Cys	Lys	Asn - `	
		410					415					420				
ACA	GAC	TCG	CGT	TGC	AAG	GCG	AGG	CAG	CTT	GAG	TTA	AAC	GAA	CGT	ACT	672
Thr	Asp	Ser	Arg	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	
	425					430					435					
TGC	AGA	TGT	GAC	AAG	CCG	AGG	CGG									696
Cys	Arg	Cys	Asp	Lys	Pro	Arg	Arg									
440					445											

- (2) INFORMATION FOR SEQ ID NO: 8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 232 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly 25 30 20

Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu 50 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val 130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr 145 150 155 160

Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp 165 170 175

Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys
180 185 190

His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn 195 200 205

Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr 210 215 220

Cys Arg Cys Asp Lys Pro Arg Arg 225 230

- (2) INFORMATION FOR SEQ ID NO: 9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

- (2) INFORMATION FOR SEQ ID NO: 10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TCCGTTTAAC TCAAGCTGCC